
M P S R C H (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jan 21 18:56:48 1997; MasPar time 820.95 Seconds
1176.812 Million cell updates/sec
Tabular output not generated.

Title: >US-08-469-637-1
Description: (1-1173) from US08469637.seq
Perfect Score: 1173
N.A. Sequence: 1 ATGAACAAGTTGCTGTGCTG.....TTTTAGAAATGATAGGTAA 1173
Comp: TACTTGTTCACGACACGAC.....AAAAATCTTTACTATCCATT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-new5
1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI
10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank94
16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7
23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5
30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2
37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2
44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1
51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8
58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1
64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8
71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4
78:VRL5 79:VRL6 80:VRL7 81:VRL8

Database: genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL

Database: u-emb146_94
96:part1

Statistics: Mean 11.363; Variance 4.199; scale 2.706

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result		Query							
No.	Score	Match	Length	DB	ID	Description	Pred. No.		
c	1	25	2.1	1441	37	S66477	glial fibrillary acid	1.02e-01	
c	2	25	2.1	1933	35	CRAGF1	Carassius auratus (GF	1.02e-01	
c	3	23	2.0	1851	54	HSLIPA4	H.sapiens LIPA gene,	2.03e+00	
c	4	23	2.0	3021	49	YSCGLN3	S.cerevisiae nitrogen	2.03e+00	
	5	24	2.0	7095	70	RRMAP1B5	R.norvegicus mRNA for	4.66e-01	
	6	23	2.0	38586	26	CELF55C12	Caenorhabditis elegan	2.03e+00	
c	7	23	2.0	43100	47	SCE9379	Saccharomyces cerevis	2.03e+00	
	8	22	1.9	1245	43	CREPHOSRI	C.reinhardtii phospho	8.43e+00	
	9	22	1.9	1256	33	OCSP17GN	O.cuniculus SP17 gene	8.43e+00	
c	10	22	1.9	1380	69	RNINL1R2A	R.norvegicus interleu	8.43e+00	
	11	22	1.9	1388	64	MMTNFR2A	M.musculus tumor necr	8.43e+00	
	12	22	1.9	1505	67	MUSMTNFR2	Mouse tumor necrosis	8.43e+00	
	13	22	1.9	2492	47	SCDNAFUS2	S.cerevisiae fus2 gen	8.43e+00	
	14	22	1.9	2552	40	I09123	Sequence 5 from paten	8.43e+00	
c	15	22	1.9	2787	69	RATPKATB5	Rat peroxisomal 3-ket	8.43e+00	
c	16	22	1.9	3112	59	HUMLD78B	Human LD78 beta gene.	8.43e+00	
	17	22	1.9	3796	68	MUSTNFR1	Murine tumor necrosis	8.43e+00	
	18	22	1.9	4561	26	CEU30248	Caenorhabditis elegan	8.43e+00	
c	19	22	1.9	7057	12	MMA1CC	Mouse mRNA for mouse	8.43e+00	
c	20	22	1.9	7057	65	MUSA1CC	Mouse mRNA for mouse	8.43e+00	
	21	22	1.9	8818	64	MMMAP1B	Mouse MAP1B mRNA for	8.43e+00	
	22	22	1.9	9416	61	HUMSEQX	Human microtubule-ass	8.43e+00	
	23	22	1.9	17013	17	EAAMASL	E.amylovara (Ea7/74)	8.43e+00	
c	24	22	1.9	28687	26	CELF42H10	C. elegans cosmid F42	8.43e+00	
	25	22	1.9	31414	26	CELC50F7	Caenorhabditis elegan	8.43e+00	
c	26	22	1.9	39307	46	SCCHXVORF	S.cerevisiae DNA for	8.43e+00	
c	27	22	1.9	40267	56	HSU159B9	Human DNA sequence fr	8.43e+00	
	28	22	1.9	40397	46	SC9959	S.cerevisiae chromoso	8.43e+00	
c	29	22	1.9	182282	80	PBU42580	Paramecium bursaria C	8.43e+00	
	30	21	1.8	774	19	HEAHI1078	Haemophilus influenza	3.30e+01	
c	31	21	1.8	814	81	VSVGINI	Vesicular stomatitis	3.30e+01	
c	32	21	1.8	2149	81	VSU13898	Vesicular stomatitis	3.30e+01	
c	33	21	1.8	2149	81	VSU12967	Vesicular stomatitis	3.30e+01	
	34	21	1.8	2305	68	RATLTNAT	Rat L-type neutral am	3.30e+01	
c	35	21	1.8	3219	38	A07457	Nucleotide sequence 1	3.30e+01	
c	36	21	1.8	3535	2	SPC	Yeast gene for catala	3.30e+01	
c	37	21	1.8	11161	81	VSVCG	Vesicular stomatitis	3.30e+01	
c	38	21	1.8	13614	82	HIU32734	Haemophilus influenza	3.30e+01	

c	39	21	1.8	13614	10	HI32734	Haemophilus influenza	3.30e+01
c	40	21	1.8	34308	84	CEW02B12	Caenorhabditis elegans	3.30e+01
c	41	21	1.8	35955	84	CEF53B7	Caenorhabditis elegans	3.30e+01
	42	21	1.8	37617	21	MLB1790G	M.leprae genes rplL,	3.30e+01
	43	21	1.8	40897	26	CELC39D10	Caenorhabditis elegans	3.30e+01
c	44	21	1.8	42557	84	CEC11H1	Caenorhabditis elegans	3.30e+01
	45	21	1.8	144861	75	HHU43400	Human herpesvirus-7 (3.30e+01

ALIGNMENTS

RESULT 1

LOCUS S66477 1441 bp mRNA VRT 17-DEC-1993

DEFINITION glial fibrillary acidic protein {clone 2} [Cyprinus carpio=carp, brain, mRNA Partial, 1441 nt].

ACCESSION S66477

NID g435738

KEYWORDS .

SOURCE carp brain.

ORGANISM Cyprinus carpio

Unclassified.

REFERENCE 1 (bases 1 to 1441)

AUTHORS Cohen,I., Shani,Y. and Schwartz,M.

TITLE Cloning and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration

JOURNAL J. Comp. Neurol. 334 (3), 431-443 (1993)

MEDLINE 93388923

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 139069] from the original journal article. This sequence comes from Fig. 1.

FEATURES Location/Qualifiers

source 1..1441

/organism="Cyprinus carpio"

/note="carp"

CDS 1..636

/partial

/note="Description: glial fibrillary acidic protein, GFAP; Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2. GFAP"

/codon_start=1

/product="glial fibrillary acidic protein"

/db_xref="PID:g435739"

/translation="VDLDVSKPDLTTALKEIRAQFEAMATSNMQETEEWYRSKFADLT DAASRNTEALRQAKQEANEYRRQIQGLTCDLESLRGSNESLERQLREMEERFTIETAG YQDTVARLEDEIQMLKEEMARHLQEQDLLNVKLALDIEIATYRKLLEGEESRITVPV QNFTNLQFRDTS LDTKLTP EAHVKRSIVVRTVETRDGEI IKESTTERNDLP"

BASE COUNT 420 a 273 c 347 g 401 t

ORIGIN

Query Match 2.1%; Score 25; DB 37; Length 1441;

Best Local Similarity 77.8%; Pred. No. 1.02e-01;

Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 438 gaagctgctcgaaggagaggaaagcagaatcactgttccggtgca 482

Cp 886 GAAGCTGCTCGAAGGTGAGGTTAGCATGTCCAATGTGCCGCTGCA 842

RESULT 2
 LOCUS CRAGF1 1933 bp mRNA VRT 01-SEP-1993
 DEFINITION Carassius auratus (GFAP-1) mRNA, complete cds.
 ACCESSION L23876
 NID g388622
 KEYWORDS .
 SOURCE Carassius auratus adult retina cDNA to mRNA.
 ORGANISM Carassius auratus
 Eukaryota; Animalia; Chordata; Vertebrata; Osteichthyes;
 Actinopterygii; Cypriniformes; Cyprinoidei; Cyprinidae.
 REFERENCE 1 (bases 1 to 1933)
 AUTHORS Glasgow, E. and Schechter, N.
 TITLE Nucleotide sequence of a GFAP - like intermediate filament cDNA
 from Goldfish retina
 JOURNAL Unpublished (1993)
 FEATURES Location/Qualifiers
 source 1..1933
 /organism="Carassius auratus"
 /dev_stage="adult"
 /sequenced_mol="cDNA to mRNA"
 /tissue_type="retina"